

# SHARP: a Smart Hierarchical Algorithm to Register Psoriasis\*

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**Abstract** – A In this work, an automatic algorithm for registering psoriasis images is proposed. The algorithm, made up of two stages, takes advantage of the behaviour of the disease. In the first stage, the diseased area is segmented in the image. The second stage uses this information to align the image based on the two first statistical moments of the area. The algorithm is compared with other existing methods. One of these methods was developed specifically to register psoriasis images. Results show the suitability of the proposed algorithm from the point of view of accuracy, parameter dependency and speed.

**Keywords:** Registration, change detection, exploratory analysis, mixture of Gaussians.

## I. INTRODUCTION

One of the main objectives in the field of dermatology is to detect and quantify the changes of a lesion over a period of time. However, nowadays there are no objective methods to assess the seriousness of the lesion. Physicians make scorings, typically on a five-point scale, and take notes to document the actual condition of the patient. These notes and perhaps some photographs are presently the only memory of what the lesion looked like at the corresponding patient visit.

A similar issue, in remote sensing, aims to assess the deforestation and to study the changes in vegetation in the same area through digital images collected via satellite at different times [1]. Nielsen [2] proposed the multivariate alteration detection transform to deal with this problem. This transform can be applied to dermatology images to detect changes during the evolution of the disease. However, because it requires a correspondence between pixels, a registration of the images is needed before the transform is applied.

Several research projects have been conducted in the last decade to register medical images. However, these methods are highly dependent on the images under study. A method that has been widely applied for medical registration arises from the statistical shape analysis theory [3]. In this theory, objects are described by their shape, that is all the geometrical information that remains when location, scale and rotational effects are filtered out from the object. Shapes are described by landmarks, which are correspondence points on each object that match between and within population. These landmarks can then be used to align the objects minimizing the Procrustes distance between shapes.

Nevertheless, although this method has been extensively utilized in different medical applications [4], the suitability for dermatological images is complicated. This is mainly due to the diversity and complexity that these lesions exhibit.

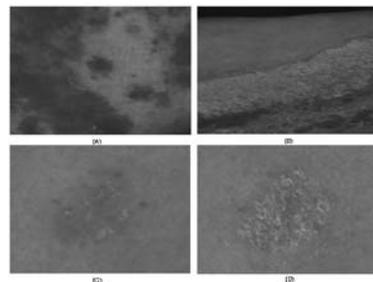


Fig. 1: Different psoriasis lesions.

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This can be appreciated in Figure 1 where four psoriasis images are shown. This disease expresses itself in thick, red areas with silvery scales [5]. Figure 1 shows the lack of suitable points to place meaningful landmarks. Points of high curvature, extremes or easily recognizable points are almost unappreciable. Furthermore, the unclear border between the lesion and normal skin makes the positioning of the landmark inaccurate.

Maletti[6] developed an algorithm to specifically register these kind of images. However, although it was showed to work fine with some images, it fails in others. This is because the algorithm registers the images based on the texture information inside the lesion.

However, this is not convenient because inside the lesion is where the images are less similar. This can be appreciated in Figure 1 (b) and (c) where the lesion has been captured at two different weeks. These images show the high variability inside the lesion. Moreover, the complexity of the algorithm and the wide search space make it quite slow.

In this work a new algorithm that takes into account the behavior of the disease is proposed to solve this problem. First the algorithm uses a mixture of Gaussians to create a binary image where the lesion is defined clearly. This binary image is used afterwards to register different images through a rigid registration by moments.

## II. THE SHARP ALGORITHM

As it has been discussed above, the psoriasis behavior is characterized by changes inside the lesion but not in the shape of the contour. The fact that the shape does not change implies that if two images of a same lesion are taken at two different times, for aligning both lesions is sufficient, "under suitable conditions", to remove the rotation and translation effects. Suitable conditions mean

that the images are collected without changing the scale. The SHARP algorithm takes these facts into account to register the psoriasis images in two stages.

### A. First stage: Segmenting the lesion

In the first stage, SHARP converts the image into a format that enhances the similarity of the images. To achieve this goal, the algorithm segments the lesion and it creates a binary image where the lesion is represented by 1 and the remaining parts of the image (normal skin, background,...) by 0. The lesion is segmented assuming that, under a good linear combination of the colour bands, the projection of the image using this combination can be represented as a mixture of two Gaussians. The parameters of these Gaussians are estimated[7] and used to separate the two classes via quadratic discriminant analysis. In the case of psoriasis, Delgado[8] showed that the combination of the green band minus the blue band allows sufficiently precise separation of the lesion.

### B. Second stage: Removing the rotation and translation effects

Once that the lesions have been formatted in a comparable way, a rigid registration by moments[9] is applied to align them. Let  $I$  be a digital image with dimension  $n_1 \times n_2$  and let  $I(x,y)$  be the intensity of the pixel  $(x,y)$ , in our case 1 or 0. The first and second order moments of the image  $I$  are calculated by:

$$E_I = \frac{\sum_{x=0}^{n_1} \sum_{y=0}^{n_2} I(x,y) [x, y]}{\sum_{x=0}^{n_1} \sum_{y=0}^{n_2} I(x,y)} \quad (1)$$

$$D_I = \frac{\sum_{x=0}^{n_1} \sum_{y=0}^{n_2} I(x,y) ([x, y] - E_I) ([x, y] - E_I)^T}{\sum_{x=0}^{n_1} \sum_{y=0}^{n_2} I(x,y)} \quad (2)$$

Let  $P_I$  be the orthogonal matrix whose columns are the eigenvectors of  $D_I$  and  $\Lambda_I$  the diagonal matrix formed with the eigenvalues such that  $D_I = P\Lambda_I^{1/2} (P\Lambda_I^{1/2})^T$ . Then if  $J(u,v)$  is another image characterized by the moments  $E_J$  and  $D_J$  with eigenvector matrix  $P_J$  and eigenvalue matrix  $\Lambda_J$ , the rigid motion  $J(u,v)=I(R[x,y]+t)$ , where  $R=P_J P_I^{-1}$  and  $t=R_J - R E_I$  gives image  $I$  the first order moment as image  $J$  and aligns the first principal components of the images.

The rotation  $R$  and translation  $t$  are then used to register the original images. In order to check that the eigenvectors are not flipped, the correlation between the images under study is verified to be positive. Otherwise,  $R$  is replaced by  $R$  rotated 180 degrees.

## III. EXPERIMENTAL RESULTS

Two experiments are conducted with the objective of showing the performance of the algorithm and testing its accuracy. The datasets used in the two studies were obtained in collaboration with the dermatological department of Gentofte Hospital in Denmark. The images of these datasets have been captured with Videometer Lab in order to guarantee that they preserve the scale.

This equipment assures even lighting and constant geometrical conditions during and between the different sessions allowing images taken at different times to be compared.

### A. Experiment 1

In The first experiment aims at showing how SHARP works and to demonstrate its accuracy. To accomplish this objective, four psoriasis images of the same lesion collected at different weeks were registered with respect to another image (reference image) of the same lesion. The reference image was captured the same day as the image of the first week. The fact that the images were collected in different weeks means that they exhibit high variation inside the lesion.

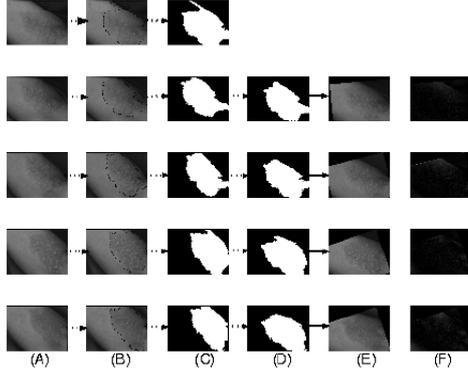


Figure 2: Row 1: reference image. Rows 2-5: registration process images week 1-4. Columns: (a) the five psoriasis images. (b) result of the segmentation (c) binary images (d) registration of the binary images (e) the original images registered (f) absolute value of the difference between the original image and the reference image.

Figure 2 shows the performance of the algorithm. In the first column, the five images selected in the experiment are displayed. The image in the first row is the reference image. The second column shows the result of the segmentation. This is used to create a binary image that is displayed in the third column. These binary images are registered with respect to the binary image of the reference image and the result is shown in the fourth column. Notice the similarity between them. The transformation applied to register the binary images is applied to the original color images and the result is displayed in the fifth column. The last column shows the difference between the fourth registered image with respect to the first one. The almost black difference image demonstrates the accuracy of the registration. The correlations between the registered images were calculated to verify this fact. It was found that the correlations were 0.825, 0.737, 0.803, 0.7025 between the images of the weeks 1 to 4, respectively, with the reference image. The high values and the fact that highest correlation appears with the two images from the same week also supports the high accuracy of the algorithm.

### B. Experiment 2

On The objective of the second experiment is to compare the performance of the SHARP algorithm with two other methods to register medical images. A general method based on landmarks and the developed specifically to register psoriasis images by Maletti. Four collections of psoriasis images were selected to measure the precision of the three different methods. Three of the

collections are made up of 20 images arranged in four groups.

Each group contains five images captured in the same week (two images were removed from one of the datasets to exactly reproduce the experiment that Maletti carried out). The last dataset is composed of 15 images arranged in 3 groups of 5 images per group. These datasets will be referred as 1A, 1B, 1C and 3C to be consistent with previous works.

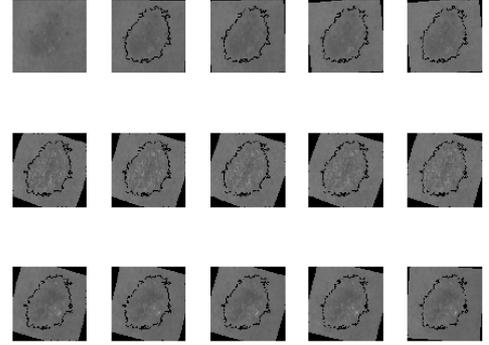


Figure 3: Result of the registration of the images of the dataset 1C with respect to the first image.

The result of applying SHARP to register this collection with respect to the first image of the first week (top left corner) is presented in Figure 3. The border of the lesion in the reference image is calculated and displayed on top of the registered images to demonstrate the effectiveness of the method.

In order to objectively compare the performance of the different algorithms the average correlation for each colour band was calculated. Let  $N$  be the number of images of the dataset  $j$  ( $j=1:4$ ) and  $b$  a colour band of a given image, the average correlation is defined as

$$\mu_{j,b} = \frac{1}{N} \sum_{i=1}^N E_{j,b,i} [corr]$$

where

$$E_{j,b,i} [corr] = \frac{1}{N-1} \sum_{w=1}^N (corr(X_{j,b,i} - Y_{j,b,w}) - 1)$$

and  $X_{j,b,i}$  represent the colour band  $b$  of the image  $i$  in dataset  $j$  and  $Y_{j,b,w}$  is the band  $b$  of the registered image  $w$  of dataset  $j$  with respect to  $X_{j,b,i}$ . The method based on landmarks performed very poorly in comparison with the other two algorithms. Due to this, the results of this method were not included in the tables. As was commented before, the reason of this poor behaviour is the lack of suitable points to place the landmarks and the difficulty to position them accurately.

Table 1 and Table 2 show that the SHARP algorithm performs better than Maletti's algorithm in three of the four collections based on the average correlation. The

reason for the inferior performance in the dataset 1A is due to the fact that some lesions in the last group of the dataset(week 4) are incomplete or affected by shadows. This means that the segmented areas differ considerably and therefore that the SHARP algorithm cannot align the axes properly. In cases where one of the lesions differs significantly from the others, an algorithm based on a

Table 1: Average correlation using Maletti's algorithm.

Dataset	$\mu_R$	$\sigma_R$	$\mu_G$	$\sigma_G$	$\mu_B$	$\sigma_B$
1A	0.68	0.04	0.56	0.05	0.36	0.05
1B	0.68	0.07	0.53	0.08	0.46	0.07
1C	0.29	0.08	0.19	0.07	0.13	0.05
3C	0.28	0.03	0.10	0.03	0.15	0.02

Table 2: Average correlation using the SHARP algorithm.

Dataset	$\mu_R$	$\sigma_R$	$\mu_G$	$\sigma_G$	$\mu_B$	$\sigma_B$
1A	0.62	0.04	0.43	0.06	0.26	0.05
1B	0.70	0.11	0.61	0.11	0.57	0.09
1C	0.40	0.03	0.29	0.03	0.25	0.02
3C	0.38	0.04	0.14	0.04	0.16	0.03

wide search, such as Maletti's is preferred, although the needed time to register the images would increase notably. However, it should be pointed out that, even in this situation, the search should be conducted using the binary images instead of the original bands.

Tables 3 and 4 show that when the average correlation is calculated using SHARP only with images from the same week, the correlation values grow significantly.

Table 3: Average correlation within weeks of the dataset 1A.

Dataset 1A	$\mu_R$	$\mu_G$	$\mu_B$
Week 1	0.82	0.76	0.62
Week 2	0.81	0.68	0.67
Week 3	0.92	0.77	0.69
Week 4	0.78	0.64	0.55

Table 4: Average correlation within weeks for the different datasets.

Datasets	$\mu_R$	$\mu_G$	$\mu_B$
1A	0.84	0.71	0.63
1B	0.71	0.63	0.61
1C	0.76	0.73	0.70
3C	0.51	0.26	0.27

Therefore, the lower correlation is a consequence of the variation inside the lesion in different weeks and this effect should be eliminated before registering the images. The above mentioned problem with the last group of the collection 1A can also be seen.

#### IV. CONCLUSIONS

In this work, a robust algorithm to register psoriasis images has been proposed. The algorithm takes advantage of the behaviour of the disease. The only needed assumption is that the images to be registered have roughly the same scale. Under this assumption, the algorithm is fully automatic. The algorithm has been compared with two other registration methods: a general-purpose registration method and one developed specifically to register this kind of images. The three methods have been applied to three data sets of psoriasis images. The task of registration in these data sets is difficult because the images in these data sets exhibit high variability and complexity. However, the obtained results demonstrate that the developed algorithm is appropriate from the point of view of accuracy, speed and parameter dependence. Although the algorithm has been tested with psoriasis images, its use to other dermatological diseases with similar behaviour is straightforward. The registered images are suitable to be subsequently utilised in chance detection.

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